

Copyright (c) 1993 - 2000 Compugen Ltd.

GenCore version 4.5

AC P09799;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE VICTILIN C72-A PRECURSOR (ALPHA-GLOBULIN A).
 OS Gossypium hirsutum (Upland cotton).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophytá; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Malvales; Malvaceae.
 RN [1]
 RP
 RA Chian C.A., Borroto K., Kamalay J.A., Dure L. III;
 RT "Developmental biochemistry of cottonseed embryogenesis and alpha
 globulin (vicilin) genes of cottonseed.";
 RL Plant Mol. Biol. 9:531-546(1987).
 CC
 CC -!- FUNCTION: SEED STORAGE PROTEIN.
 CC -!- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
 BODIES.
 CC -!- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
 CONGLICININ, ETC.).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>).
 CC [1]
 CC -----
 DR EMBL; M19378; AA033069.1; -.
 DR P06398;
 DR HSSP; P50477; ICAX.
 DR INTERPRO; IPR001113; -.
 DR PRAM; PRF0046; Seedstore_7s; 1.
 KW Seed storage protein; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 605 AA; 71049 MW; C9DB9371C976953B CRC64;
 SQ RESULT 3
 ID AGRP_LUFCY
 ID AGRP_LUFCY STANDARD
 AC P56568;
 DR 15-DEC-1998 (Rel. 37, Created)
 DR 15-DEC-1998 (Rel. 37, Last sequence update)
 DE 6.5 kDa ARGinine/Glutamate-rich Polypeptide (6.5k-AGRP).
 OC Luffa cylindrica (smooth loofah).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophytá; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Cucurbitales; Cucurbitaceae; Luffa.
 RN [1]
 RP
 RC TISSUE-SEED;
 RX MEDLINE=9737433; PubMed=9214759;
 RA Kimura M., Park S.S., Sakai R., Yamasaki N., Funatsu G.;
 RT Primary structure of 6.5-k-arginine/glutamate-rich polypeptide from
 the seeds of sponge gourd (luffa cylindrica).";
 RL Biosci. Biotechnol. Biochem. 61: 984-988(1997).
 CC -!- FUNCTION: STORAGE PROTEIN WHICH PROVIDES NITROGEN AND CARBON
 CC RESERVES DURING GERMINATION AND SEEDLING GROWTH.
 CC -!- MASS SPECTROMETRY: MW=5693.39; METHOD=MALDI.

CC -!- SIMILARITY: SOME, TO 7S SEED STORAGE PROTEINS.
 KW Seed storage protein.
 FT DISULFID 12 33
 FT DISULFID 16 29
 SEQUENCE 47 AA; 5698 MW; 588B0EC82273AC05 CRC64;
 SQ Query Match 31.5%; Score 78; DB 1; Length 47;
 Best Local Similarity 40.0%; Pred. No. 0.028;
 Matches 14; Conservative 9; Mismatches 8; Indels 4; Gaps 1;
 SEQUENCE 47 AA; 5698 MW; 588B0EC82273AC05 CRC64;
 SQ Query Match 31.5%; Score 78; DB 1; Length 47;
 Best Local Similarity 40.0%; Pred. No. 0.028;
 Matches 14; Conservative 9; Mismatches 8; Indels 4; Gaps 1;
 SEQUENCE 47 AA; 5698 MW; 588B0EC82273AC05 CRC64;
 SQ Query Match 31.5%; Score 78; DB 1; Length 47;
 Best Local Similarity 40.0%; Pred. No. 0.028;
 Matches 14; Conservative 9; Mismatches 8; Indels 4; Gaps 1;
 SEQUENCE 47 AA; 5698 MW; 588B0EC82273AC05 CRC64;

RESULT 4
 ID Y551-CABEL
 ID STANDARD
 ID PRM; 154 AA.
 AC Q0962;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HYPOTHEICAL 15.6 kDa PROTEIN ZR673.1 IN CHROMOSOME II PRECURSOR.
 GN ZR673.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA McMURRAY A.;
 RL Submitted (Mar-1995) to the EMBL/GenBank/DDBJ databases.
 RN (2)
 RP REVISIONS.
 RC STRAIN-BRISTOL N2;
 RA Jones S.J.M.;
 RL Submitted (Nov-1997) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: STRONG, TO C. ELEGANS E04D5.4 AND SOME, TO C. ELEGANS
 C03G6.13.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>).
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; 248585; CAA88486.1;
 DR HSSP; P01551; ICAX.
 DR WORMPEP; ZK673.1; CEL6742.
 KW Hypothetical protein; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 154 HYPOTHEICAL PROTEIN ZR673.1.
 SQ SEQUENCE 154 AA; 15637 MW; 323A02C3A2E782AB CRC64;

Query Match 27.0%; Score 67; DB 1; Length 154;
 Best Local Similarity 35.5%; Pred. No. 0.95; Mismatches 15; Indels 0; Gaps 0;
 Matches 11; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

RESULT 5
 ID ANDR_HUMAN
 ID ANDR_HUMAN STANDARD
 AC P10275;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)

- DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).
GN AR OR NR3C4 OR DHTR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [11]
RP SEQUENCE FROM N.A.
RX MEDLINE=89112208; PubMed=3216866;
RA Lubahn D.B., Joseph D.R., Sar M., Tan J., Higgs H.N., Larson R.E.,
RA French F.S., Wilson E.M.;
RT "The human androgen receptor: complementary deoxyribonucleic acid
RT cloning, sequence analysis and gene expression in prostate.",
RA Mol. Endocrinol. 2:1265-1275(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90063302; PubMed=2594783;
RA Lubahn D.B., Brown T.R., Simental J.A., Higgs H.N., Migeon C.J.,
RA Wilson E.M., French F.S.;
RT "Sequence of the intron/exon junctions of the coding region of the
RT human androgen receptor gene and identification of a point mutation
RT in a family with complete androgen insensitivity.",
Proc. Natl. Acad. Sci. U.S.A. 86:9534-9538(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90256935; PubMed=2342476;
RA Govindan M.V.;
RT "Specific region in hormone binding domain is essential for hormone
RT binding and trans-activation by human androgen receptor.",
RL Mol. Endocrinol. 4:411-427(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RX MEDLINE=89107168; PubMed=3174628;
RA Chang C., Kountis J., Liao S.;
RT "Structural analysis of complementary DNA and amino acid sequences of
RT human and rat androgen receptors.",
Proc. Natl. Acad. Sci. U.S.A. 85:7211-7215(1988).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RX MEDLINE=89098909; PubMed=2911578;
RA Tilley W.D., Marcelli M., Wilson J.D., McPhaul M.J.;
RT "Characterization and expression of a cDNA encoding the human androgen
RT receptor.",
Proc. Natl. Acad. Sci. U.S.A. 86:327-331(1989).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RX MEDLINE=9155943; PubMed=2293020;
RA Marcelli M., Tilley W.D., Wilson C.M., Griffin J.E., Wilson J.D.,
MCPhaul M.J.;
RT "Definition of the human androgen receptor gene structure permits the
RT identification of mutations that cause androgen resistance: premature
termination or the receptor protein at amino acid residue 588 causes
RT complete androgen resistance.",
RL Mol. Endocrinol. 4:1105-1116(1990).
RN [7]
RP SEQUENCE OF 189-919 FROM N.A.
RX MEDLINE=89178111; PubMed=3353726;
RA Chang C., Kokontis J., Liao S.;
RT "Molecular cloning of human and rat complementary DNA encoding
RT androgen receptors.",
Science 240:324-326(1988).
RN [8]
RP SEQUENCE OF 468-919 FROM N.A.
RX MEDLINE=882610407; PubMed=3377788;
RA Trapman J., Klaassen P., Kuiper G.G.J.M., van der Korput J.A.G.M.,
Faber P.W., van Rooij H.C.J., Geurts van Kessel A., Voorhorst M.M.,
RA Mulder E., Brinkmann A.O.;
RT "Cloning, structure and expression of a cDNA encoding the human
androgen receptor.",
Biochem. Biophys. Res. Commun. 153:241-248(1988).
RN [9]
RP POLYMORPHISM OF POLY-GLN REGION.
RX MEDLINE=92220629; PubMed=1561105;
RA Sleddens H.F., Oostra B.A., Brinkmann A.O., Trapman J.;
RT "Trinucleotide repeat polymorphism in the androgen receptor gene
(AR).";
RL Nucleic Acids Res. 20:1427-1427(1992).
RN [10]
RP POLYMORPHISM OF POLY-GLY REGION.
RX TISSUE=BLOOD;
RA Lu J., Danielseen M.;
RT "Androgen receptor gene mutations in X-linked spinal and bulbar
muscular atrophy.",
Nature 352:77-79(1991).
RN [11]
RP VARIANT SBMA IN POLY-GLN REGION.
RX MEDLINE=91287825; PubMed=2062380;
RA La Spada A.R., Wilson E.M., Lubahn D.B., Harding A.E., Fischbeck
Patterson M.N., Hughes L.A., Gottlieb B., Pinsky L.;
RT "Androgen receptor gene mutations in X-linked spinal and bulbar
muscular atrophy.",
Nature 352:77-79(1991).
RN [12]
RP REVIEW ON VARIANTS.
RX MEDLINE=95023089; PubMed=7937057;
RA Gottlieb B., Trifiro M., Lumbruso R., Gottlieb B., Pinsky L.;
RT "The androgen receptor gene mutations database.",
Nucleic Acids Res. 22:3560-3562(1994).
RN [13]
RP REVIEW ON VARIANTS.
RX MEDLINE=97169385; PubMed=9016528;
RA Gottlieb B., Trifiro M., Lumbruso R., Vasiliou D.M., Pinsky L.;
RT "The androgen receptor gene mutations database.",
Nucleic Acids Res. 25:158-162(1997).
RN [14]
RP VARIANT LNCAP ALA-877.
RX MEDLINE=9103633; PubMed=2260966;
RA Veldscholte J., Ruis-Stalpers C., Kuiper G.G., Jenster G.,
Bertrevoets C., Claassen E., van Rooij H.C.J., Trapman J.,
RA Brinkmann A.O., Mulder E.;
RT "A mutation in the ligand binding domain of the androgen receptor of
human LNCAP cells affects steroid binding characteristics and
response to anti-androgens.",
J. Steroid Biochem. Biophys. Res. Commun. 173:534-540(1990).
RN [15]
RP VARIANT CA1S MET-866.
RX MEDLINE=9118593; PubMed=2082179;
RA Brown T.R., Lubahn D.B., Wilson E.M., French F.S., Migeon C.J.,
Confer J.L.;
RT "Functional characterization of naturally occurring mutant androgen
receptors from subjects with complete androgen insensitivity.",
Mol. Endocrinol. 4:1759-1772(1990).
RN [16]
RP VARIANT CYS-774.
RX MEDLINE=91310758; PubMed=1856263;
RA Marcelli M., Tilley W.D., Zoppi S., Griffin J.E., Wilson J.D.,
MCPhaul M.J.;
RT "Androgen resistance associated with a mutation of the androgen
receptor at amino acid 772 (Arg-->Cys) results from a combination of
decreased messenger ribonucleic acid levels and impairment of
receptor function.",
J. Clin. Endocrinol. Metab. 73:318-325(1991).
RN [17]
RP VARIANT CA1S ASN-695 AND HIS-695, AND SEQUENCE OF 629-723 FROM N.A.
RX MEDLINE=92131007; PubMed=1775137;
RA Ruis-Stalpers C., Trifiro M.A., Kuiper G.G., Jenster G., Romalo G.,
Sal T., van Rooij H.C., Kaufman M., Rosenthal R.L., Liao S.;
RT "Substitution of aspartic acid-686 by histidine or asparagine in the
human androgen receptor leads to a functionally inactive protein with
altered hormone-binding characteristics.",
Mol. Endocrinol. 5:1562-1569(1991).
RN [18]
RP VARIANT CA1S AND PA1S.
RX MEDLINE=9338440; PubMed=1307250;
RA Batch J.A., Williams D.M., Davies H.R., Brown B.D., Evans B.A.J.,
Hughes I.A., Patterson M.N.;

RT	"Androgen receptor gene mutations identified by SSPC in fourteen subjects with androgen insensitivity syndrome.";	RN	Hum. Mol. Genet. 1:497-503(1992);	RP	
RL	VARIANT CAIS VAL-787.	RT	[19]	RL	
RX	MDLINV=9225226; Published=1569163;	RA	Fukumaki Y., Nawata H.;	CC	SEQUENCE FROM N.A.
RA	"A single amino acid substitution (Met-786->Val) in the steroid-binding domain of human androgen receptor leads to complete androgen insensitivity syndrome.";	RA	Choong C.S., Kemppainen J.A., Wilson E.M.;	CC	MDLINV=88404153; PubMed=9732460;
RT	J. Clin. Endocrinol. Metab. 74:1152-1157(1992).	RT	"Evolution of the primate androgen receptor: a structural basis for disease.";	CC	Choong C.S., Kemppainen J.A., Wilson E.M.;
RT	[201]	RL	J. Mol. Evol. 47:334-342(1998).	CC	-!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EURYKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
RT	VARIANT LNCAP ALA-877.	CC	-!- SUBCELLULAR LOCATION: NUCLEAR.	CC	-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
RT	MDLINV=9222955; Published=1562539;	CC	A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.	CC	-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
RP	VARIANT MET-730.	CC	NR3 SUBFAMILY.	CC	
RX	MDLINV=9235229; Published=1631125;	CC		CC	
RA	Weldschlotte J., Berrevoets C.A., Ris-Stalpers C., Kuiper G.G., Jenster G., Trapman J., Brinkmann A.O., Mulder E.;	CC		CC	
RA	"The androgen receptor in LNCAP cells contains a mutation in the ligand binding domain which affects steroid binding characteristics and response to antiandrogens.";	CC		CC	
RT	R.L. Steroid Biochem. Mol. Biol. 41:665-669(1992).	CC		CC	
RN	[21]	CC		CC	
RP	VARIANT MET-730.	CC		CC	
RX	MDLINV=93372806; Published=8103398;	CC		CC	
RA	Isaacs W.B., Brown T.R., Barrack E.R.; Newmark J.R., Hardy D.O., Carter B.S., Epstein J.L., Isaacs W.B., Brown T.R., Barrack E.R.; Proc. Natl. Acad. Sci. U.S.A. 89:6319-6323(1992).	CC		CC	
RA	"Androgen receptor gene mutations in human prostate cancer.";	CC		CC	
RT	Proc. Natl. Acad. Sci. U.S.A. 89:6319-6323(1992).	CC		CC	
RL	[22]	CC		CC	
RN	VARIANT CAIS VAL-754.	CC		CC	
RX	MDLINV=93372806; Published=8103398;	CC		CC	
RA	Llobatcerro J.-M., Lumbrosa S., Kiarri R., Dumas R., Sultan C.; Ibanez J.-M., Lumbrosa S., Kiarri R., Dumas R., Sultan C.;	CC		CC	
RA	"An exonic point mutation creates a MaefII site in the androgen receptor gene of a family with complete androgen insensitivity syndrome.";	CC		CC	
RT	Proc. Natl. Acad. Sci. U.S.A. 90:6328-6332(1993).	CC		CC	
RL	[23]	CC		CC	
RN	VARIANT CAIS ARG-807.	CC		CC	
RX	MDLINV=94108430; Published=8281140;	CC		CC	
RA	Adeyemo O., Kallilio P.J., Palvimo J.J., Kontula K., Jaenne O.A.; Adeyemo O., Kallilio P.J., Palvimo J.J., Kontula K., Jaenne O.A.;	CC		CC	
RT	"A single-base substitution in exon 6 of the androgen receptor gene causing complete androgen insensitivity: the mutated receptor fails to transactivate but binds to DNA in vitro.";	CC		CC	
RT	Hum. Mol. Genet. 2:1809-1812(1993).	CC		CC	
RL	[24]	CC		CC	
RN	VARIANT PATS VAL-743.	CC		CC	
RX	MDLINV=9335568; Published=8325932;	CC		CC	
RA	Nakao R., Yanase T., Sakai Y., Haji M., Nawata H.;	CC		CC	
RT	"A single amino acid substitution (Gly743 -> Val) in the steroid-binding domain of the human androgen receptor leads to Reifenstein syndrome.";	CC		CC	
RT	Query Match 26.2%; Score 65; DB 1; Length 919; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		CC	
Matches 14; Conservative 6; Mismatches 9; Indels 0; Gaps 0;	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 30	CC		
Db 61 0000000000000000ETSPRQQQQ 89	Db	61 0000000000000000ETSPRQQQQ 86	CC		
RESULT 6	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT	Query Match 25.8%; Score 64; DB 1; Length 911; Best Local Similarity 50.0%; Pred. No. 7.9; Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;	CC		
ANDR_PANT	STANDARD:	OY	2 QEDPQTECQCQCRRCQQESGRQQCQ 27	CC	
ID ANDR_PANT	PRT; 911 AA.	Db	61 0000000000000000ETSPRQQQQ 86	CC	
RESULT 7	RT				

RA	Duvick J.P., Roord T., Rao A.G., Marshak D.R., RT
"PURIFICATION AND CHARACTERIZATION OF A NOVEL ANTIMICROBIAL PEPTIDE FROM MAIZE (<i>Zea mays L.</i>) KERNELS."	RL
J. BIOL. CHEM. 267:18814-18820(1992).	CC
-!- FUNCTION: INHIBITOR OF BOTH BACTERIAL AND FUNGAL GROWTH IN VITRO.	CC
-!- TISSUE SPECIFICITY: PREDOMINANTLY IN THE EMBRYO PORTION OF THE KERNEL.	CC
P1R: AA1822; AA1822.	DR
MAIZE DB: 69182; -	KW
Fungicide; Antibiotic	SQ
SEQUENCE 33 AA: 4131 MW: B148F1B90E823599 CRC64;	
RESULT 8	Query Match
HSP1_MOUSE	Best Local Similarity 25.6%; Score 63.5; DB 1; Length 33;
ID HSP1_MOUSE	Matches 11; Conservative 44.0%; Pred. No. 0 64; Mismatches 6; Indels 1; Gaps 1;
AC F02319;	DB 6 ECRRQCLRRHEGQPWETQECMRRCR 30
DT 21-JUL-1986 (REL. 01, Created)	
DT 21-JUL-1986 (REL. 01, Last sequence update)	
DT 15-DEC-1998 (REL. 37, Last annotation update)	
DE SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).	
GN PRM1 OR PRM1.	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
RN [1]	
SEQUENCE FROM N A.	
RX MEDLINE=85199803; PubMed=2986694;	
RA Kleene R.C., Distel R.J., Hecht N.B.;	
RT "Nucleotide sequence of a cDNA clone encoding mouse protamine 1.";	
RL Biochemistry 24:719-722(1985).	
RN [2]	
SEQUENCE FROM N A.	
RX MEDLINE=88193085; PubMed=3358932;	
RA Johnson P.A., Peschon J.J., Yelick P.C., Palmiter R.D., Hecht N.B.;	
RT "Sequence homologies in the mouse protamine 1 and 2 genes.";	
RL Biochim. Biophys. Acta 950:45-53(1988).	
RN [3]	
SEQUENCE FROM N A.	
RX MEDLINE=87260978; PubMed=303751;	
RA Peschon J.J., Behringher R.R., Brinster R.L., Palmiter R.D.;	
RT "Spermatid-specific expression of protamine 1 in transgenic mice.";	
RL Proc. Natl. Acad. Sci. U.S.A. 84:5316-5319(1987).	
RN [4]	
SEQUENCE FROM N A.	
RX MEDLINE=88181903; PubMed=3445973;	
RA Hecht N.B.;	
RT "Gene expression during spermatogenesis.";	
RL Ann. N.Y. Acad. Sci. 513:90-101(1987).	
RN [5]	
SEQUENCE FROM N A.	
RC STRAIN=C129;	
RA Schlueter G., Engel W.;	
RT Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.	
RL -!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF	
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT	
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.	
CC -!- SUBUNIT: CROSS-LINKED BY INTERCHAIN DISULFIDE BONDS AROUND THE	
CC DNA-HELIX (BY SIMILARITY).	
CC -!- SUBCELLULAR LOCATION: NUCLEAR.	
CC -!- TISSUE SPECIFICITY: TESTIS.	
CC	
CC	
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	

RX MEDLINE:76184789; PubMed=1268226; RA Kistler W.S.; Keim P.S.; Heintzner R.L.; RT Partial structural analysis of the basic chromosomal protein of rat spermatozoa";
 RL Biochim. Biophys. Acta 427:752-757(1976).
 CC -!- FUNCTION: PROTEAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
 CC -!- SUBUNIT: CROSS-LINED BY INTERCHAIN DISULFIDE BONDS AROUND THE DNA-HELIX (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- TISSUE SPECIFICITY: TESTIS.
 CC
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 DR EMBL; 246939; CAM87061_1; -.
 DR PIR; A2712; A27128.
 DR PIR; S03997; S03997.
 DR INTERPRO; IPR000221; -.
 DR PFAM; PF00260; protamine_PI; 1.
 DR PROSITE; PS00048; PROTAMINE_PI; 1.
 KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
 KW Testis; DNA condensation; Nuclear protein.
 FT INIT-MET 0 0
 FT DISULFID 5 5
 FT DISULFID 6 14
 FT DISULFID 21 21
 FT DISULFID 36 36
 FT DISULFID 37 47
 SQ SEQUENCE 50 AA; 6889 MW; B60B9F3D1BB6D978 CRC64;
 RESULT 10
 KAPC_DICDI ID_KAPC_DICDI STANDARD; PRT; 648 AA.
 AC P34099;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT (EC 2.7.1.37).
 GN PKAC OR PK2 OR PK3.
 OC Dictyostelium discoideum (Slime mold);
 OC Eukaryota; Dictyostellida; Dictyostelium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:91323730; PubMed=1864510;
 RA Bierki E., Anjard C., Schoder J.-C., Raymond C.D.;
 RT "Isolation of two genes encoding putative protein kinases regulated during Dictyostelium discoideum development.;"
 RL Gene 102:57-65(1991).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE:93305090; PubMed=8373760;
 RA Anjard C., Etchebehere L., Pinaud S., Veron M., Raymond C.D.;
 RT "An unusual catalytic subunit for the camp-dependent protein kinase of Dictyostelium discoideum.;"
 RL Biochemistry 32:9532-9538(1993).
 [3]

RP CHARACTERIZATION.
 RC STRAIN=AX3;
 RC MEDLINE=93066311; PubMed=133205;
 RA Mann S. K.O., Yonemoto W.M., Taylor S.S., Firtel R.A.;
 RT "DdkP3, which plays essential roles during Dictyostelium development, encodes the catalytic subunit of cAMP-dependent protein kinase.;"
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10701-10705(1992);
 CC -!- FUNCTION: ESSENTIAL FOR DIFFERENTIATION AND FRUIT MORPHOGENESIS.
 CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.
 CC -!- SUBUNIT: IN DICTYOSTELIUM THE HOLOENZYME IS A DIMER COMPOSED OF A REGULATORY (R) AND A CATALYTIC (C) SUBUNIT. IN THE PRESENCE OF CAMP IT DISSOCIATES INTO THE ACTIVE C SUBUNIT AND AN R MONOMER.
 CC -!- DEVELOPMENTAL STAGE: CAPK ACTIVITY IS LOW IN VEGETATIVELY GROWING AMOEBAE, INCREASES DURING DEVELOPMENT OF AGGREGATION AND REACHES A MAXIMUM AT CUMULATION.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMP SUBFAMILY.
 CC
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M38703; -; NOT_ANNOTATED_CDS.
 DR PIR; J01150; J01150.
 DR HSSP; P05132; ZCPK.
 DR DICTYDB; DD02030; PRKC.
 DR INTERPRO; IPR000719; -.
 DR INTERPRO; IPR000961; -.
 DR INTERPRO; IPR002290; -.
 DR PFAM; PF00069; Pkinase; 1.
 DR PFAM; PF0443; Pkinase_C; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferease; Serine/threonine-protein kinase; ATP-binding; cAMP; Phosphorylation.
 FT DOMAIN 58 64 ASN-RICH.
 FT DOMAIN 136 223 GLN-RICH.
 FT DOMAIN 233 250 THR-RICH.
 FT DOMAIN 336 590 PROTEIN KINASE.
 FT NP_BIND 342 350 ATP (BY SIMILARITY).
 FT BINDING 365 365 ATP (BY SIMILARITY).
 FT ACT_SITE 459 459 BY SIMILARITY.
 FT MOD_RES 490 490 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 648 AA; 74458 MW; D0F5B3A4AC58D084 CRC64;
 RESULT 11
 ANDR_CANFA ID_ANDR_CANFA STANDARD; PRT; 907 AA.
 AC Q9T50;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DB 145 QQQPQQQQPQQQQPQQQQPQQQQPQQQLQQNQQQQ 185
 DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).
 GN AR OR NR3C4.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN

DR	EMBL; M34442; AAA30853.1; -.
DR	INTERPRO; IPR002360; -.
KW	PROSITE; PS00795; INVOLCRIN; 1.
KW	Keratinocyte; Repeat;
SQ	SEQUENCE 285 AA; 33384 MW; DCE1BD88B9248BEA CRC64;
RESULT 14	NRH3_MOUSE
ID	NRH3_MOUSE STANDARD; PRT; 445 AA.
AC	Q9Z0Y9; 30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DR	OXYSTEROIDS RECEPTOR LXR-ALPHA (LIVER X RECEPTOR ALPHA) (NUCLEAR ORPHAN RECEPTOR LXR-ALPHA).
DE	NRL3 OR LXXA.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=LIVER;
RX	MEDLINE=92262897; PubMed=7744246;
RA	Willy P.-J., Umesono K., Ong E.S., Evans R.M., Heyman R.A., Mangelsdorf D.J.;
RA	RTR "LXR, a nuclear receptor that defines a distinct retinoid response pathway.", Genes Dev., 9:1033-1045(1995).
RL	CC SHIFT RXR FROM ITS ROLE AS A SILENT DNA-BINDING PARTNER TO AN ACTIVE LIGAND-BINDING SUBUNIT IN MEDIATING RETINOID RESPONSES THROUGH TARGET GENES DEFINED BY LXRES.
CC	--!- SUBUNIT: INTERACTS WITH RXR.
CC	--!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC	--!- INDUCTION: BY 9-CIS RETINOIC ACID (ICRA).
CC	--!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC	NRL1 SUBFAMILY.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licensee@isb-sib.ch).
CC	DR EMBL; U02662; AAA8556.1; -.
CC	DR HSSP; P20393; 1A6Y.
CC	DR MIM; 602423; -.
CC	DR INTERPRO; IPR00536; -.
CC	DR INTERPRO; IPR001628; -.
CC	DR PFAM; PF00104; hormone_rec; 1.
CC	DR PFAM; PF00105; zf-C4; 1.
CC	DR PRINTS; PR00047; STROIDFINGER.
CC	DR PROSITE; PS00031; NUCLEAR_RECEPтор; 1.
CC	KW Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger.
CC	KW Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger.
CC	KW Zinc-finger.
FT	DNA_BIND 96 161 C4-TYPE ZINC FINGERS (TWO).
FT	ZN_FING 96 116 C4-TYPE.
FT	ZN_FING 132 156 C4-TYPE.
SQ	SEQUENCE 445 AA; 50480 MW; IAA27B233B0F8C96 CRC64;
Query Match	Best local similarity 39.0%; Score 59; DB 1; Length 445; Matches 16; Conservative 10; Mismatches 5; Indels 10; Gaps 4;
Query Match	Best local similarity 39.0%; Score 59; DB 1; Length 447; Matches 16; Conservative 10; Mismatches 5; Indels 10; Gaps 5;
Qy	8 ECQQCQ-RRCRQDQESPRQQYC-----QRCKETCEEEE 42
Db	147 KCQCERLRKCRQ--AGMEE--CVLSEEQIRKLKKRQEEE 183
Query Match	Best local similarity 39.0%; Score 59; DB 1; Length 445; Matches 16; Conservative 10; Mismatches 5; Indels 10; Gaps 4;
Query Match	Best local similarity 39.0%; Score 59; DB 1; Length 447; Matches 16; Conservative 10; Mismatches 5; Indels 10; Gaps 4;
Qy	8 ECQQCQ-RRCRQDQESPRQQYC-----QRCKETCEEEE 42
Db	149 KCQCERLRKCRQ--AGMEE--CVLSEEQIRKLKKRQEEE 185